

Genome version 4.5
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OM protein - protein search, using SW model

Run on: January 17, 2002, 08:00:09 : Spent 0 min 23.78 Seconds

With 10000 alignments
5,555 million cell updates/sec

Title: us-09-674-436-1

Percent score: 25

Sequence: 1 BLK6 5

Scoring Method: P080962

Gap: 10.0, Gapex: 0.5

Search: 522453 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 622453

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

Database:

A_Geneseq.1011*

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22: 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	Pos	Ident
1	25	100.0	5	21	AAV75478
2	25	100.0	5	22	AAV75478
3	25	100.0	124	21	AAV75478
4	25	100.0	127	21	AAV75478
5	25	100.0	142	21	AAV75478
6	25	100.0	158	16	AAV75478
7	25	100.0	179	14	AAV75478
8	25	100.0	180	17	AAV75478
9	25	100.0	181	15	AAV75478
10	25	100.0	186	21	AAV75478
11	25	100.0	186	21	AAV75478

12	25	100.0	187	21	AAV75478
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Query Match	100.00%	Score 250	100.00%	100.00%	100.00%
Fast Local Similarity	100.00%	Prod. No. 10	2	100.00%	100.00%
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cy	1 DLRG 5				
lt	1111				
lt	96 dlrq 100				
Result	5				
AA12725					
lt	AA12725 standard; Proteins: 10 AA				
xx					
AA	AA12725:				
xx					
AA	17-007-2000 (first entry)				
xx					
xx	Arabidopsis thaliana protein fragment: Sg... N... (100.00%)				
xx					
xx	Protein identification: signal transduction factor 1, 100.00% (100.00%)				
xx	hybridization assay: no match in query database (100.00%)				
xx	to match: sequence				
xx					
xx	Arabidopsis thaliana				
xx					
xx	EP1033405-A2				
xx					
xx	06-SEP-2000:				
xx					
xx	25-FEB-2000: 2000EP1033405-A2				
xx					
xx	25-FEB-1999:	991S-012127			
xx	05-MAR-1999:	991S-012130			
xx	09-MAR-1999:	991S-012415			
xx	23-MAR-1999:	991S-012508			
xx	25-MAR-1999:	991S-012509			
xx	29-MAR-1999:	991S-012518			
xx	01-APR-1999:	991S-012761			
xx	06-APR-1999:	991S-012834			
xx	08-APR-1999:	991S-012811			
xx	16-APR-1999:	991S-012915			
xx	19-APR-1999:	991S-013007			
xx	21-APR-1999:	991S-013243			
xx	23-APR-1999:	991S-013310			
xx	23-APR-1999:	991S-013301			
xx	28-APR-1999:	991S-013419			
xx	30-APR-1999:	991S-013204			
xx	30-APR-1999:	991S-013217			
xx	04-MAY-1999:	991S-013281			
xx	05-MAY-1999:	991S-013285			
xx	06-MAY-1999:	991S-013286			
xx	06-MAY-1999:	991S-013287			
xx	07-MAY-1999:	991S-013283			
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xx	27-MAY-1999:	991S-013632			
xx	28-MAY-1999:	991S-013732			
xx	01-JUN-1999:	991S-013732			
xx	03-JUN-1999:	991S-013738			
xx	04-JUN-1999:	991S-013702			
xx	07-JUN-1999:	991S-013721			
xx	08-JUN-1999:	991S-013804			
xx	10-JUN-1999:	991S-013814			

[illegible]

PE 03-FEB-1994: 94W0-A000047.
 XX
 PR 03-FEB-1994: 94W0-000719Z.
 XX
 PA (AMBA-) AMBAV (ORP) LTD.
 XX
 PI Gough NM 147736 M1 Metcalf E. New LA MO. 050000K M1
 XX
 DK WPI: 1994-279689/34.
 XX
 PI New receptor-binding determinants from leuko-10 inhibitory
 PI factor useful for designing analogues
 XX
 PS Disclosures: Fig.4: 55pp: English.
 XX
 CC The sequences of mouse (AA66150), human (AA66151) and pig (AA66152)
 CC LIF proteins and of human G-CSF (AA66132) were sequenced. Novel
 CC receptor-binding determinants are based on the human LIF
 CC sequence.
 XX
 SO Sequence: 181 AA.

Query Match: 100.0% Score: 25; 19.1; 10.0; 10.0; 10.0
 Best Local Similarity: 100.0%; 19.1; 10.0; 10.0; 10.0
 Matches: 5; Conserved: 0; Mismatches: 0; Gaps: 0
 GY 1 11111 5
 DI 121 diff: 125

RESULT 11

AAV75463
 ID AAV75463 standard: protein: 186 AA
 XX
 AC AAV75463:
 XX
 DI 21-MAR-2000 (first entry)
 XX
 DE Neisseria meningitidis ORF 714 protein sequence. See US Patent.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic diagnosis; immunogenic; infect; anti-infectious; prophylaxis;
 KW antibacterial; gene therapy.
 XX
 OS Neisseria meningitidis
 XX
 PN W09957280-A2.
 XX
 PU 11-Nov-1999.
 XX
 PE 30-APR-1999: 99W0-05093446.
 XX
 PR 01-MAY-1998: 98US-0084758.
 PR 31-JUL-1998: 98US-0094869.
 PR 02-SEP-1998: 98US-0094894.
 PR 02-SEP-1998: 98US-0099062.
 PR 09-OCT-1998: 98US-0107449.
 PR 09-OCT-1998: 98US-0107474.
 PR 09-OCT-1998: 98US-0107494.
 PR 09-OCT-1998: 98US-0107496.
 PR 25-FEB-1999: 99US-0121528
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO) INST GEN-MIC RES.
 XX
 PI Fraser C, Gallooli C, Gandhi G, Hickey L, Lee Paul V, Mada M,
 PI Petersen J, Fizza M, Rappelli R, Rathi G, Zeng D, Zeng S, Zeng M,
 PI Telleche H, Walter JG.
 XX
 WPI: 2000-062159/05.
 DR R F508, AA651225.
 XX

PI Novel Neisserial polypeptides produced by recombinant gene for
 PI vaccines and diagnostics
 XX
 ES Claim 2: Page 115; 1454pp: English.
 XX
 CC AA651015 to AA651016, AA651017 to AA651018, and AA651019 to AA651020
 CC represent novel Neisserial polypeptides and the amino acid sequences
 CC and polypeptides, AA651021 to AA651026 and AA651027 to AA651032 represent
 CC the primers used in the amplification of the present invention. The
 CC polypeptides, the polypeptides, and the amino acid sequences, and the
 CC the invention can be used as vaccines, as diagnostic reagents, and as
 CC immunogenic compositions. The polypeptides can be used in the
 CC manufacture of medications for treatment of present and future
 CC Neisserial bacteria (see mutations and recombination) to produce the
 CC presence of Neisserial bacteria or to treat and prevent the
 CC be used to screen for mutants or to detect and identify the
 CC have also be used in gene therapy protocols. The polypeptides of the invention
 CC may also be used in gene therapy protocols.

XX
 SO Sequence: 186 AA.

Query Match: 100.0% Score: 25; 19.1; 10.0; 10.0; 10.0
 Best Local Similarity: 100.0%; 19.1; 10.0; 10.0; 10.0
 Matches: 5; Conserved: 0; Mismatches: 0; Gaps: 0
 GY 1 11111 5
 DI 5 diff: 9

RESULT 12

AAV75464
 ID AAV75464 standard: protein: 186 AA
 XX
 AC AAV75464:
 XX
 DI 21-MAR-2000 (first entry)
 XX
 DE Neisseria meningitidis ORF 714 protein sequence. See US Patent.
 XX
 KW Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;
 KW antigenic diagnosis; immunogenic; infect; anti-infectious; prophylaxis;
 KW antibacterial; gene therapy.
 XX
 OS Neisseria meningitidis
 XX
 PN W09957280 A2.
 XX
 PU 11-Nov-1999.
 XX
 PE 30-APR-1999: 99W0-05093446.
 XX
 PR 01-MAY-1998: 98US-0084758.
 PR 31-JUL-1998: 98US-0094869.
 PR 02-SEP-1998: 98US-0094894.
 PR 02-SEP-1998: 98US-0099062.
 PR 09-OCT-1998: 98US-0107449.
 PR 09-OCT-1998: 98US-0107474.
 PR 09-OCT-1998: 98US-0107494.
 PR 09-OCT-1998: 98US-0107496.
 PR 25-FEB-1999: 99US-0121528
 XX
 PA (CHIR) CHIRON CORP.
 PA (GENO) INST GEN-MIC RES.
 XX
 PI Fraser C, Gallooli C, Gandhi G, Hickey L, Lee Paul V, Mada M,
 PI Petersen J, Fizza M, Rappelli R, Rathi G, Zeng D, Zeng S, Zeng M,
 PI Telleche H, Walter JG.
 XX
 WPI: 2000-062159/05.
 DR R F508, AA651226.
 XX
 PI Novel Neisserial polypeptides produced by recombinant gene for

XX Sequence 194 AAs

Query Match: 100.0%; Score 25; Id 1; Length 194;
Best Local Similarity: 100.0%; Pctd. No. 1; Id 1;
Matches 5; Conservative 0; Mismatches 0; Gaps 0

QY 1 D1160 5
1 111
DB 121 d1160 126

RESULT 15

AA75345
ID AA75345 standard; Protein: 194 AAs.

XX AA75345;

XX 13-DEC-1995 (first entry)

XX Hybrid human cytokine IL1E.

XX Hybrid cytokine; tumour proliferation; cancer therapy.

XX Synthetic.

XX Key: Location/Qualifiers

XX Misc-difference 132 /note "site of stop codon"

XX W09513444-A.

XX 18-MAY-1995.

XX 07-NOV-1994; 94WO-051287A.

XX 08-NOV-1994; 94US-0149101.

XX (HUT-) HUTCHINSON CANCER RES CENTER ERHD.

XX Leung JW, Rose TM, Tedaro GJ;

XX WPT: 1995-194111/25.

XX N-PSDB: AA75345.

XX New hybrid cytokines with alpha helical segments from different sources - also DNA encoding them, vectors and T-activated cells, useful e.g. for treating cancer, remodeling tissue.

XX Claim 11: Page 33-34; 52pp; English.

XX The cytokine encoding genes for leukemia inhibitory factor (LIF), granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6), interleukin-11 (IL-11), ciliary neurotrophic factor (CNTF) and oncostatin M (OS) have been cloned and reported in the literature.

XX LIF, G-CSF, IL-6, IL-11, and CNTF each comprise four alpha-helical sequences. In each cytokine, the four alpha-helical sequences are linked by non-

XX alpha-helical "linker" sequences of about 5-10 AAs. The invention

XX provides a group of therapeutic hybrid cytokines having a size range

XX from about 10 to about 30 kDa. Each hybrid cytokine comprises three or

XX four alpha-helical sequences and linker sequences, ranging from about

XX 5-40 AAs in length. In the nomenclature of the hybrid cytokines,

XX upper case letters designate alpha-helical segments, lower case

XX letters (whether Arabic numerals, alphabetic or symbolic) indicate

XX a specific linker sequence. The first three alpha-helical

XX alpha-sequences were derived from IL-11.

XX Sequence 194 AAs

Best Local Similarity: 100.0%; Score 25; Id 1; Length 194;
Matches 5; Conservative 0; Mismatches 0; Gaps 0

QY 1 D1160 5
1 111
DB 121 d1160 126

Search completed: January 22, 2002 07:43:15
Job Time: 509 sec

Query Match

100.0%; Score 25; Id 1; Length 194;

GenCode version 4.5
Copyright (c) 1993 - 2000 GenCode Ltd.

OM Protein Protein search, using SW model

Run on: January 17, 2002, 08:02:04 : 2000.4.100.12.47 seconds

261 total alignments
7024 alignment cell updates/sec

Header:

US-09-674-436-1

Sequence:

1 01186 5

Scoring table:

BLAST/BLAST2
Gapop: 10.0, Gapext: 0.5

Scored: 21252 steps, 2500000 residues

Total number of hits satisfying chosen parameters: 21252

Minimum DB seq length: 3

Maximum DB seq length: 200000000

Post-processed: Minimum Match: 0.8

Maximum Match: 100%

Listing first 45 summaries

Database:

Issued: Patents.AA*

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2: US-08-076-087-1
3: US-08-111-224-1
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5: US-08-076-087-1
6: US-08-076-087-1
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27: US-08-076-087-1

Prep. No. is the number of results provided by chance to have a score greater than or equal to the result being returned, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
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3	25	100.0	179	US-08-111-224-1	Sequence 1, April
4	25	100.0	179	PCT-US94-076-087-1	Sequence 1, April
5	25	100.0	181	US-08-076-087-1	Sequence 2, April
6	25	100.0	181	US-08-076-087-1	Sequence 2, April
7	25	100.0	181	US-08-076-087-1	Sequence 2, April
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42	25	100.0	182	US-09-674-436-1	Sequence 4, April
43	25	100.0	182	US-09-674-436-1	Sequence 4, April
44	25	100.0	182	US-09-674-436-1	Sequence 4, April
45	25	100.0	182	US-09-674-436-1	Sequence 4, April

ALIGNMENTS

RESULT 1

US-08-378-617A-42

Sequence 32, Application N/0806617A

GENERAL INFORMATION:

APPLICANT: 1 Aptos, Acton, MA

APPLICANT: 1 Aptos, Acton, MA

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APPLICANT: 1 Aptos, Acton, MA

APPLICANT: 1 Aptos, Acton, MA

28	25	100.0	182	US-09-674-436-1	Sequence 4, April
29	25	100.0	182	US-09-674-436-1	Sequence 4, April
30	25	100.0	182	US-09-674-436-1	Sequence 4, April
31	25	100.0	182	US-09-674-436-1	Sequence 4, April
32	25	100.0	182	US-09-674-436-1	Sequence 4, April
33	25	100.0	182	US-09-674-436-1	Sequence 4, April
34	25	100.0	182	US-09-674-436-1	Sequence 4, April
35	25	100.0	182	US-09-674-436-1	Sequence 4, April
36	25	100.0	182	US-09-674-436-1	Sequence 4, April
37	25	100.0	182	US-09-674-436-1	Sequence 4, April
38	25	100.0	182	US-09-674-436-1	Sequence 4, April
39	25	100.0	182	US-09-674-436-1	Sequence 4, April
40	25	100.0	182	US-09-674-436-1	Sequence 4, April
41	25	100.0	182	US-09-674-436-1	Sequence 4, April
42	25	100.0	182	US-09-674-436-1	Sequence 4, April
43	25	100.0	182	US-09-674-436-1	Sequence 4, April
44	25	100.0	182	US-09-674-436-1	Sequence 4, April
45	25	100.0	182	US-09-674-436-1	Sequence 4, April

US-08-378-617A-42

Sequence 32, Application N/0806617A

GENERAL INFORMATION:

APPLICANT: 1 Aptos, Acton, MA

APPLICANT: 1 Aptos, Acton, MA

APPLICANT: 1 Aptos, Acton, MA

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APPLICANT: 1 Aptos, Acton, MA

APPLICANT: 1 Aptos, Acton, MA

TOPOLGY: Linear
PCT-US91-07759-1

Query Match 100.0% Score 25; 18 4 Length 181;
Best Local Similarity 100.0% Prod. No. 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DILRG 5
DB 119 DILRG 123

RESULT 5

US-08-505-187-2
Sequence 2 Application: US/08505187
Patent No. 6184370

GENERAL INFORMATION:

APPLICANT: Layton, Meredith J.

OWZAREK, Catherine M.

Nicola, Nicos A.

Gough, Nicholas M.

Metcalfe, Donald

TITLE OF INVENTION: ELECTRO-BINDING OF A NANOPARTICLE

LEUKAEMIA INHIBITOR BY FACTOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seattle, Scott, Murphy & Co. Inc.

STREET: 400 Garden City Plaza

CITY: Garden City

STATE: New York

COUNTRY: USA

ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Vector 0 #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/505,187

FILING DATE: 27-Sep-1995

CLASSIFICATION: <unknown>

AUTHOR/AGENT INFORMATION:

NAME: DIGITAL, Frank S.

REGISTRATION NUMBER: 31,316

REFERENCE/DOCKET NUMBER: 9792

TELEPHONE: (516)742-4343

TELEFAX: (516)742-4366

TELEX: 240 901 SANS UR

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 181 amino acids

TYPE: amino acid

STANDARDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2

Query Match 100.0% Score 25; 18 4 Length 181;
Best Local Similarity 100.0% Prod. No. 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DILRG 5
DB 121 DILRG 125

RESULT 6
5187077-27
Patent No. 5187077

APPLICANT: GEARING, DAV. P.; GORDON, NICHOLAS J.;
NICHOLAS J. KING, JILLIE A. METCALFE, DONALD
NICHOLAS, NICO A.; GORDON, NICHOLAS J.; GEARING, DAV. P.
TITLE OF INVENTION: LEUKAEMIA INHIBITOR BY FACTOR
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
ACCESSION NUMBER: U9759294.1
FILING DATE: 09-SEP-1998
SEQ ID NO: 27
LENGTH: 181

5187077-27

Query Match 100.0% Score 25; 18 4 Length 181;
Best Local Similarity 100.0% Prod. No. 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DILRG 5
DB 61 DILRG 65

RESULT 7

Patent No. 5427925

APPLICANT: GEARING, DAV. P.; GORDON, NICHOLAS J.

NICHOLAS J. KING, JILLIE A. METCALFE, DONALD

NICHOLAS, NICO A.; GORDON, NICHOLAS J.; GEARING, DAV. P.

TITLE OF INVENTION: LEUKAEMIA INHIBITOR BY FACTOR

NUMBER OF SEQUENCES: 4

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 5427925

FILING DATE: 06-MAR-1994

APPLICATION NUMBER: 948,614

FILING DATE: 22-SEP-1992

APPLICATION NUMBER: 607,159

FILING DATE: 11-MAR-1991

SEQ ID NO: 25

LENGTH: 181

5427925-25

Query Match 100.0% Score 25; 18 4 Length 181;
Best Local Similarity 100.0% Prod. No. 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DILRG 5
DB 61 DILRG 65

RESULT 8

US-08-149-101A-24

Sequence 24, Application: US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Jodaro, George J.

APPLICANT: Jodaro, George J.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSER: CGL Technologies, Inc.

STREET: 200 El Centro Avenue West, Suite 4

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 14MB, double sided, both densities

OPERATING SYSTEM: MS-DOS Version 6

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Generation version 4.1.
Copyright (c) 1993 - 2000 J. M. J. Coen, Ltd.

protein search, using SW model

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Run on:      January 17, 2002, 08:09:14 : 507.01 sec (12.91 seconds)
              (with 1000000 updates/sec)
              9.502 M.illion cell updates/sec
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FIGURE 10

Sequences: 1 MILK; 2

Scoring table: HUSUM62

Category	Value
Category 10.0	Category 10.0
Category 10.5	Category 10.5

Source: *Journal of the American Medical Association*, 1964, 191: 1231-1232.

Total number of hits satisfying chosen parameters 41924)

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Minimum DB Seq length: 0
Maximum DB Seq length: 2000000000
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Post-process time:	Minimum match ok
	Maximum Match 100%
Listing first 45 summaries	

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Database :
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *
```

pred. R. is the number of responses predicted to have to have a score greater than or equal to the score of a result being predicted, and is verified by analysis of the total score, is 144000.

SUMMARY

Result No.	Score	* Query Match	Length	DB	ID	Accession
1	25	100.0	116	2	T15604	hypothetical protein
2	25	100.0	148	2	E82873	ribosomal protein
3	25	100.0	159	2	PC4109	conserved hypothetical
4	25	100.0	160	2	E82191	conserved hypothetical
5	25	100.0	172	2	G81015	probable aminoacyl-tRNA synthetase
6	25	100.0	186	2	D81119	conserved hypothetical
7	25	100.0	186	2	D81961	hypothetical protein
8	25	100.0	193	2	S83414	hypothetical protein
9	25	100.0	197	2	B64410	hypothetical protein
10	25	100.0	202	1	P36292	serine ribonuclease
11	25	100.0	203	2	G85288	hypothetical protein
12	25	100.0	203	2	T05519	hypothetical protein
13	25	100.0	244	2	T28319	hypothetical protein
14	25	100.0	249	2	G69681	hypothetical protein
15	25	100.0	252	2	E63469	hypothetical protein
16	25	100.0	251	2	E81992	hypothetical protein
17	25	100.0	292	2	G81848	RNA methylase, RrmA
18	25	100.0	310	2	H75153	Spd methylase, RsmA
19	25	100.0	338	2	H65022	thiamine nucleoside phosphorylase
20	25	100.0	349	2	G71849	hypothetical protein
21	25	100.0	349	2	G64475	hypothetical protein
22	25	100.0	398	2	H72565	hypothetical protein
23	25	100.0	391	2	G82522	hypothetical protein
24	25	100.0	396	2	A70641	hypothetical protein
25	25	100.0	416	2	T75334	probable Hbb protein
26	25	100.0	439	2	S52589	hypothetical protein
27	25	100.0	440	2	H86842	phosphotransferase
28	25	100.0	441	2	A82781	hypothetical protein
29	25	100.0	441	2	A41791	transport protein

[illegible][illegible][illegible]

Society Month	Feb-Mar	Score	257	144	113
Best Local Singing	Oct-Nov	Fried No. 1			100%
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	111				
Ob	49 Little 53				

[illegible]

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RA Henley D., Scheel P.: The EHL, 2000, 211-214, 215-216, 217-218, 219-220, 221-222, 223-224, 225-226, 227-228, 229-230, 231-232, 233-234, 235-236, 237-238, 239-240, 241-242, 243-244, 245-246, 247-248, 249-250, 251-252, 253-254, 255-256, 257-258, 259-260, 261-262, 263-264, 265-266, 267-268, 269-270, 271-272, 273-274, 275-276, 277-278, 279-280, 281-282, 283-284, 285-286, 287-288, 289-290, 291-292, 293-294, 295-296, 297-298, 299-300, 301-302, 303-304, 305-306, 307-308, 309-310, 311-312, 313-314, 315-316, 317-318, 319-320, 321-322, 323-324, 325-326, 327-328, 329-330, 331-332, 333-334, 335-336, 337-338, 339-340, 341-342, 343-344, 345-346, 347-348, 349-350, 351-352, 353-354, 355-356, 357-358, 359-360, 361-362, 363-364, 365-366, 367-368, 369-370, 371-372, 373-374, 375-376, 377-378, 379-380, 381-382, 383-384, 385-386, 387-388, 389-390, 391-392, 393-394, 395-396, 397-398, 399-400, 401-402, 403-404, 405-406, 407-408, 409-410, 411-412, 413-414, 415-416, 417-418, 419-420, 421-422, 423-424, 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Figure 1 is a schematic representation of the experimental design. It shows a flow from 'Study 1' to 'Study 2'. Study 1 involves 'Pretest' and 'Main Study'. Study 2 involves 'Pretest' and 'Main Study'. The 'Main Study' in both studies involves 'Participants' and 'Conditions'.

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The following are the values of A , B , C , D , E , F , G , H , I , J , K , L , M , N , O , P , Q , R , S , T , U , V , W , X , Y , Z , AA , AB , AC , AD , AE , AF , AG , AH , AI , AJ , AK , AL , AM , AN , AO , AP , AQ , AR , AS , AT , AU , AV , AW , AX , AY , AZ , BA , BB , BC , BD , BE , BF , BG , BH , BI , BJ , BK , BL , BM , BN , BO , BP , BQ , BR , BS , BT , BU , BV , BW , BX , BY , BZ , CA , CB , CC , CD , CE , CF , CG , CH , CI , CJ , CK , CL , CM , CN , CO , CP , CQ , CR , CS , CT , CU , CV , CW , CX , CY , CZ , DA , DB , DC , DD , DE , DF , DG , DH , DI , DJ , DK , DL , DM , DN , DO , DP , DQ , DR , DS , DT , DU , DV , DW , DX , DY , DZ , EA , EB , EC , ED , EE , EF , EG , EH , EI , EJ , EK , EL , EM , EN , EO , EP , EQ , ER , ES , ET , EU , EV , EW , EX , EY , EZ , FA , FB , FC , FD , FE , FF , FG , FH , FI , FJ , FK , FL , FM , FN , FO , FP , FQ , FR , FS , FT , FU , FV , FW , FX , FY , FZ , GA , GB , GC , GD , GE , GF , GG , GH , GI , GJ , GK , GL , GM , GN , GO , GP , GQ , GR , GS , GT , GU , GV , GW , GX , GY , GZ , HA , HB , HC , HD , HE , HF , HG , HH , HI , HJ , HK , HL , HM , HN , HO , HP , HQ , HR , HS , HT , HU , HV , HW , HX , HY , HZ , IA , IB , IC , ID , IE , IF , IG , IH , II , IJ , IK , IL , IM , IN , IO , IP , IQ , IR , IS , IT , IU , IV , IW , IX , IY , IZ , JA , JB , JC , JD , JE , JF , JG , JH , JI , IJ , JK , JL , JM , JN , JO , JP , JQ , JR , JS , JT , JU , JV , JW , JX , JY , JZ , KA , KB , KC , KD , KE , KF , KG , KH , KI , KJ , KL , KM , KN , KO , KP , KQ , KR , KS , KT , KU , KV , KW , KX , KY , KZ , LA , LB , LC , LD , LE , LF , LG , LH , LI , LJ , LK , LL , LM , LN , LO , LP , LQ , LR , LS , LT , LU , LV , LW , LX , LY , LZ , MA , MB , MC , MD , ME , MF , MG , MH , MI , MJ , MK , ML , MM , MN , MO , MP , MQ , MR , MS , MT , MU , MV , MW , MX , MY , MZ , NA , NB , NC , ND , NE , NF , NG , NH , NI , NJ , NK , NL , NM , NN , NO , NP , NQ , NR , NS , NT , NU , NV , NW , NX , NY , NZ , OA , OB , OC , OD , OE , OF , OG , OH , OI , OJ , OK , OL , OM , ON , OO , OP , OQ , OR , OS , OT , OU , OV , OW , OX , OY , OZ , PA , PB , PC , PD , PE , PF , PG , PH , PI , PJ , PK , PL , PM , PN , PO , PP , PQ , PR , PS , PT , PU , PV , PW , PX , PY , PZ , QA , QB , QC , QD , QE , QF , QG , QH , QI , QJ , QK , QL , QM , QN , QO , QP , QQ , QR , QS , QT , QU , QV , QW , QX , QY , QZ , RA , RB , RC , RD , RE , RF , RG , RH , RI , RJ , RK , RL , RM , RN , RO , RP , RQ , RR , RS , RT , RU , RV , RW , RX , RY , RZ , SA , SB , SC , SD , SE , SF , SG , SH , SI , SJ , SK , SL , SM , SN , SO , SP , SQ , SR , SS , ST , SU , SV , SW , SX , SY , SZ , TA , TB , TC , TD , TE , TF , TG , TH , TI , TJ , TK , TL , TM , TN , TO , TP , TQ , TR , TS , TT , TU , TV , TW , TX , TY , TZ , UA , UB , UC , UD , UE , UF , UG , UH , UI , UJ , UK , UL , UM , UN , UO , UP , UQ , UR , US , UT , UU , UV , UW , UX , UY , UZ , VA , VB , VC , VD , VE , VF , VG , VH , VI , VJ , VK , VL , VM , VN , $$

[illegible]

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration was adjusted to 10⁸ cells/ml. The cells were then mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The asterisk indicates a significant difference (p < 0.05) between the two strains.

[illegible][illegible]

the other side of the road from the "Baptist Church." It is a small, old building, with a porch, and a sign on the front that reads "The Methodist Church." The sign is made of wood, and has the words "The Methodist Church" written on it in a simple, bold font. The building is made of brick, and has a gabled roof. There are some trees in front of the building, and a small garden. The building is surrounded by a fence, and there is a path leading to the entrance. The building is in good condition, and it looks like it has been well-maintained. The sign is a little faded, but it is still legible. The building is a good example of a small, local church building. It is a nice addition to the neighborhood, and it is a good place for people to go to church. The building is a good example of a small, local church building. It is a nice addition to the neighborhood, and it is a good place for people to go to church.

[illegible]

Keywords: children; adolescents; parents; teachers; self-esteem; social skills

```

QY 1 DILLIG 5
DB 128 DILLIG 127

RESULT 9
YC47_HELPJ
ID YC47_HELPJ STANDARD PRI 440 AA
AC Q92542
DT 30-MAY-2000 (rel. 39, annotated)
DI 30-MAY-2000 (rel. 39, last sequence update)
DT 20-AUG-2001 (rel. 40, last annotation update)
DE PROTEIN HP1247.
GN HP1247.
OS Helicobacter pylori (Campylobacter pylori)
OC Bacteria; Proteobacteria; epsilon subdivision; helicobacter group;
OC Helicobacter;
OX NCBI_TaxID=85963
KN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:99120557, PubMed 992622.
RA Alm R.A., Ling L., Siles Molt D.E., King B.L. from Lab. Biol. P.C.
RA Smith D.R., Norman B., Guild H.C., deGange H., Daniel G.,
RA Lumma P.J., Ceruso A., Hild-Nickelset M., F. L. S. D. M., Ives P.,
KA Gibson K., Metherell D., Mills S.D., Jiang J., F. L. S. D. M., Ives G.P.,
KA Trust J.O.
RT "Genomic sequence comparison of two unrelated isolates of the human
RT gastric pathogen Helicobacter pylori."
RL Nature 397:176-180(1999)
KN [2]
RP INTERACTION.
KA Leontina F.
RL Unpublished observations (Apr-2000).
CC -1- FUNCTION: COULD BE THE FUNCTIONAL EQUIVALENT OF ENA POLYPEPTASE 111
CC DELTA SUBUNIT (HNA).
CC -1- SUBUNIT: SEEMS TO INTERACT WITH H. PYLORI HNA.
CC*
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CC
CC EMBL: A0001541; AAD06742.1
CC
CC Translated RNA directed RNA polymerase, ENA subunit.
CC Complete proteome.
CC
CC SPOUNCE 340 AA; 39544 MW; 68039PI27224016 (P0064)

```

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Query Match 100.0% Score 250 AB Length 440
Best local Similarity 100.0% Pred. No. 672
Matches 52 conservative by Mismatch 1 100.0% by Date 0
CC 1 DILLIG 5
DB 250 DILLIG 254

```

```

RESULT 10
YC47_HELPJ
ID YC47_HELPJ STANDARD PRI 440 AA
AC Q92542
DT 30-MAY-2000 (rel. 39, annotated)
DT 30-MAY-2000 (rel. 39, last sequence update)
DT 20-AUG-2001 (rel. 40, last annotation update)
DE PROTEIN HP1247.
GN HP1247.
OS Helicobacter pylori (Campylobacter pylori)
OC Bacteria; Proteobacteria; epsilon subdivision; helicobacter group;
OC Helicobacter;
OX NCBI_TaxID=85963

```

```

OX NCBI_TaxID=85963
QY 1 DILLIG 5
DB 250 DILLIG 254

RESULT 11
YC47_HELPJ
ID YC47_HELPJ STANDARD PRI 440 AA
AC Q92542
DT 30-MAY-2000 (rel. 39, annotated)
DI 30-MAY-2000 (rel. 39, last sequence update)
DT 20-AUG-2001 (rel. 40, last annotation update)
DE PROTEIN HP1247.
GN HP1247.
OS Helicobacter pylori (Campylobacter pylori)
OC Bacteria; Proteobacteria; epsilon subdivision; helicobacter group;
OC Helicobacter;
OX NCBI_TaxID=85963
KN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:97694467, PubMed 97521052.
RA Lomb J.-P., White G., Kottmann A.H., O'Leary J.A., Saito Y.,
KA Prosser J., Kottmann A.H., O'Leary J.A., Saito Y.,
KA Nelson K., Kottmann A.H., O'Leary J.A., Saito Y.,
KA Lottus B., Richardson B., Jackson K., Kottmann A.H., O'Leary J.A.,
KA McKenney K., Kottmann A.H., O'Leary J.A., Saito Y.,
KA Berg D.E., O'Leary J.A., O'Leary J.A., Kottmann A.H., O'Leary J.A.,
KA O'Leary J.A., Kottmann A.H., O'Leary J.A., Saito Y.,
KA Hayes W.S., Kottmann A.H., O'Leary J.A., Saito Y.,
KA Verter J.O.
RT "The complete genome sequence of the gastric pathogen
RT Helicobacter pylori."
RL Nature 388:760-764(1997)
KN [2]
RP INTERACTION.
KA Leontina F.
RL Unpublished observations (Apr-2000).
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CC DELTA SUBUNIT (HNA).
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CC*
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CC
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CC
CC Translated RNA directed RNA polymerase, ENA subunit.
CC Complete proteome.
CC
CC SPOUNCE 340 AA; 39544 MW; 68039PI27224016 (P0064)

```

```

Query Match 100.0% Score 250 AB Length 440
Best local Similarity 100.0% Pred. No. 672
Matches 52 conservative by Mismatch 1 100.0% by Date 0
CC 1 DILLIG 5
DB 250 DILLIG 254

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RESULT 11
YC47_HELPJ
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AC Q92542
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CC Translated RNA directed RNA polymerase, ENA subunit.
CC Complete proteome.
CC
CC SPOUNCE 340 AA; 39544 MW; 68039PI27224016 (P0064)

```


[illegible][illegible]

[illegible]

DR 10R NMB2028; -
KW Kinasol; fructiferos; completo perfume;
SU SEQUENCE 172 AA; 18946 MW; 2430296291415; 196642

